

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
S1	2	WO-9632106-\$.did.	EPO; DERWENT	OR	OFF	2006/08/09 10:55
S2	1	"4840915".pn.	USPAT	OR	OFF	2006/08/09 10:56
S3	1	"4486538".pn.	USPAT	OR	OFF	2006/08/09 10:57
S4	1	"4298590".pn.	USPAT	OR	OFF	2006/08/09 10:58
S5	52	Bogoch.in.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT	OR	OFF	2006/08/09 10:59
S6	12	aglycoprotein	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT	OR	ON	2006/08/09 11:00
S7	45	antimalignin OR (malignin AND antibody)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT	OR	ON	2006/08/09 11:01
S8	32	S5 AND (S6 OR S7)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT	OR	ON	2006/08/09 11:02

10/642,587 STN STRATEGY

(FILE 'HOME' ENTERED AT 14:56:35 ON 09 AUG 2006)

FILE 'MEDLINE, BIOSIS, LIFESCI, EMBASE, SCISEARCH, CAPLUS'
ENTERED AT

14:56:59 ON 09 AUG 2006

L1	0 S BOGOCH/AU
L2	5 S BOGOCH
L3	10 S AGLYCOPROTEIN
L4	91 S MALIGNIN
L5	58 DUP REM L4 (33 DUPLICATES REMOVED)
L6	40 S L5 AND ANTIBODY
L7	4 S AGLYCO AND 10B
L8	3 DUP REM L7 (1 DUPLICATE REMOVED)
L9	44 S GLYCOPROTEIN AND 10B
L10	31 DUP REM L9 (13 DUPLICATES REMOVED)

10/642,587 Sequence search
08/09/2006
Public databases

SEQ ID NO: 1

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	100.0	16	3	AAy87638	Aay87638 Human bra
2	85	100.0	16	5	ABG94714	Abg94714 Glioma re
3	85	100.0	16	6	ABU57264	Abu57264 Replikin
4	85	100.0	16	7	ADD88337	Add88337 Human mal
5	85	100.0	16	7	ADG18115	Adg18115 Glioma Re
6	85	100.0	16	9	ADW92264	Adw92264 Isolated
7	64	75.3	15	2	AAW15757	Aaw15757 Peptide f
8	52	61.2	10	5	ABG94733	Abg94733 Glioma re
9	52	61.2	10	6	ABU57283	Abu57283 Replikin
10	52	61.2	10	9	ADW92283	Adw92283 Malignin
11	51	60.0	10	5	ABG94711	Abg94711 Glioma re
12	51	60.0	10	5	ABG94793	Abg94793 Replikin
13	51	60.0	10	6	ABU57343	Abu57343 Replikin
14	51	60.0	10	6	ABU57261	Abu57261 Replikin
15	51	60.0	10	7	ADD88416	Add88416 Cancer ce

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	100.0	16	2	US-09-146-755-1	Sequence 1, Appli
2	85	100.0	16	2	US-09-817-144-1	Sequence 1, Appli
3	46	54.1	717	2	US-09-487-558B-376	Sequence 376, App
4	46	54.1	738	2	US-09-538-092-575	Sequence 575, App
5	43	50.6	464	2	US-09-050-739-62	Sequence 62, Appl
6	43	50.6	464	2	US-09-804-980-62	Sequence 62, Appl
7	43	50.6	474	2	US-08-311-731A-353	Sequence 353, App
8	42	49.4	236	2	US-09-270-767-56840	Sequence 56840, A
9	42	49.4	313	2	US-09-252-991A-31437	Sequence 31437, A
10	40.5	47.6	465	2	US-10-029-180-44	Sequence 44, Appl
11	40	47.1	219	2	US-09-107-532A-5590	Sequence 5590, Ap
12	40	47.1	223	2	US-09-248-796A-24488	Sequence 24488, A
13	39.5	46.5	477	2	US-10-029-180-54	Sequence 54, Appl
14	39	45.9	199	2	US-10-101-464A-694	Sequence 694, App
15	39	45.9	235	2	US-09-252-991A-16701	Sequence 16701, A

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	100.0	16	3	US-09-984-056-4	Sequence 4, Appli
2	85	100.0	16	3	US-09-984-057-4	Sequence 4, Appli
3	85	100.0	16	3	US-09-817-144-1	Sequence 1, Appli
4	85	100.0	16	4	US-10-105-232-4	Sequence 4, Appli
5	85	100.0	16	4	US-10-189-437-4	Sequence 4, Appli
6	85	100.0	16	4	US-10-642-587-1	Sequence 1, Appli
7	85	100.0	16	5	US-10-860-050-4	Sequence 4, Appli
8	74.5	87.6	17	5	US-10-860-050-866	Sequence 866, App
9	52	61.2	10	5	US-10-860-050-23	Sequence 23, Appl
10	51	60.0	10	3	US-09-984-056-1	Sequence 1, Appli
11	51	60.0	10	3	US-09-984-056-83	Sequence 83, Appl
12	51	60.0	10	3	US-09-984-057-1	Sequence 1, Appli
13	51	60.0	10	3	US-09-984-057-83	Sequence 83, Appl
14	51	60.0	10	4	US-10-105-232-1	Sequence 1, Appli
15	51	60.0	10	4	US-10-105-232-83	Sequence 83, Appl

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	44	51.8	2014	7	US-11-299-791-18	Sequence 18, Appl
2	42	49.4	50	6	US-10-953-349-36303	Sequence 36303, A
3	42	49.4	170	7	US-11-056-355B-21194	Sequence 21194, A
4	42	49.4	170	7	US-11-056-355B-49330	Sequence 49330, A
5	42	49.4	170	7	US-11-056-355B-105131	Sequence 105131,
6	42	49.4	170	7	US-11-056-355B-116370	Sequence 116370,
7	42	49.4	262	7	US-11-056-355B-21193	Sequence 21193, A
8	42	49.4	262	7	US-11-056-355B-49329	Sequence 49329, A
9	42	49.4	262	7	US-11-056-355B-105130	Sequence 105130,
10	42	49.4	262	7	US-11-056-355B-116369	Sequence 116369,
11	41	48.2	80	7	US-11-056-355B-25462	Sequence 25462, A
12	41	48.2	80	7	US-11-056-355B-37890	Sequence 37890, A
13	41	48.2	80	7	US-11-056-355B-42910	Sequence 42910, A
14	41	48.2	80	7	US-11-056-355B-43439	Sequence 43439, A
15	41	48.2	97	7	US-11-056-355B-25461	Sequence 25461, A

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	48	56.5	468	2	AG2899	dihydrolipoamide d
2	48	56.5	468	2	H97674	dihydrolipoamide d
3	47	55.3	532	2	AC3359	dihydrolipoamide d
4	46	54.1	738	1	S51380	protein kinase STE
5	45	52.9	280	2	JU0294	levansucrase gene
6	45	52.9	336	2	D42653	dihydrolipoamide d
7	43	50.6	321	2	C81746	peptide ABC transp
8	43	50.6	464	2	B70828	hypothetical prote
9	43	50.6	467	2	G87207	dihydrolipoamide d
10	43	50.6	481	2	AB2753	dihydrolipoamide d
11	43	50.6	481	2	H97533	dihydrolipoamide d
12	42	49.4	262	2	T52310	Lil3 protein [impo
13	42	49.4	350	2	G71445	hypothetical prote
14	41	48.2	105	2	G89993	hypothetical prote
15	41	48.2	222	2	C89944	conserved hypothet

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	48	56.5	468	2	Q2K3F8_RHIET	Q2k3f8 rhizobium e
2	48	56.5	468	2	Q8UC66_AGRT5	Q8uc66 agrobacteri
3	48	56.5	468	2	Q98ED5_RHILO	Q98ed5 rhizobium l
4	47	55.3	481	2	Q2K8W2_RHIET	Q2k8w2 rhizobium e
5	47	55.3	486	2	Q6G167_BARQU	Q6g167 bartonella
6	47	55.3	486	2	Q6G402_BARHE	Q6g402 bartonella
7	47	55.3	487	2	Q57D13_BRUAB	Q57d13 brucella ab
8	47	55.3	487	2	Q8G0G9_BRUSU	Q8g0g9 brucella su
9	47	55.3	487	2	Q2YPV6_BRUA2	Q2ypv6 brucella ab
10	47	55.3	532	2	Q8YHE4_BRUME	Q8yhe4 brucella me
11	46	54.1	187	2	Q9EV54_RHIME	Q9ev54 rhizobium m
12	46	54.1	462	2	Q74HV2_LACJO	Q74hv2 lactobacill
13	46	54.1	467	2	Q5YNX4_NOCFA	Q5ynx4 nocardia fa
14	46	54.1	481	2	Q92Q96_RHIME	Q92q96 rhizobium m
15	46	54.1	481	2	Q98MY4_RHILO	Q98my4 rhizobium l

NA ENCODING SEQ ID NO: 1

SUMMARIES

Result	No.	Score	Query		DB	ID	Description
			Match	Length			
	1	55	64.7	218983	11	AC171274	AC171274 Gallus ga
c	2	55	64.7	225652	11	AC169087	AC169087 Gallus ga
	3	53	62.4	94320	5	AC002564	AC002564 Homo sapi
	4	53	62.4	152145	12	AC069570	AC069570 Homo sapi
	5	53	62.4	162023	5	AC147027	AC147027 Pan trogl
	6	53	62.4	177687	12	AC093321	AC093321 Homo sapi
	7	53	62.4	187139	5	AC161021	AC161021 Pan trogl
	8	53	62.4	189756	5	AC161472	AC161472 Pan trogl
	9	52	61.2	110000	15	CP000250_39	Continuation (40 o
	10	52	61.2	125713	6	AL670928	AL670928 Mouse DNA
c	11	51	60.0	160299	12	AC150969	AC150969 Bos tauru
c	12	51	60.0	173326	12	AC151220	AC151220 Bos tauru
	13	51	60.0	217285	12	AC126317	AC126317 Rattus no
c	14	51	60.0	260760	12	AC127861	AC127861 Rattus no
	15	50	58.8	79355	12	AC021280	AC021280 Homo sapi

SUMMARIES

Result	No.	Score	Query		DB	ID	Description
			Match	Length			
	1	48	56.5	1395	13	ADS62510	Ads62510 Bacterial
	2	48	56.5	1395	13	ADS62902	Ads62902 Bacterial
	3	48	56.5	1395	13	ADS59449	Ads59449 Bacterial
	4	48	56.5	1407	13	ADS60067	Ads60067 Bacterial
c	5	47.5	55.9	23603	13	ABD33391	Abd33391 Murine ca
c	6	47	55.3	5233	8	AAD55425	Aad55425 Human FGF
c	7	47	55.3	33352	9	ADA02846	Ada02846 Human FGF
c	8	47	55.3	33352	10	ADB72584	Adb72584 Human FGF
c	9	47	55.3	33352	10	ADC85325	Adc85325 Mouse Fgf
c	10	47	55.3	33352	12	ADM74441	Adm74441 Human car
c	11	47	55.3	35558	14	ADZ12667	Adz12667 Human can
	12	47	55.3	117754	11	ACN43866	Acn43866 Human gen
c	13	47	55.3	127943	12	ADQ97651	Adq97651 Human can
c	14	46	54.1	793	8	ABZ52278	Abz52278 Aspergill
	15	46	54.1	1446	13	ADS59836	Ads59836 Bacterial

SUMMARIES

Result	No.	Score	Query		DB	ID	Description
			Match	Length			
c	1	47	55.3	17352	3	US-09-949-016-12990	Sequence 12990, A
c	2	47	55.3	218940	3	US-09-949-016-17539	Sequence 17539, A
	3	46	54.1	2154	3	US-09-487-558B-375	Sequence 375, App
	4	44	51.8	348	3	US-09-621-976-12993	Sequence 12993, A
c	5	44	51.8	2415	3	US-10-104-047-730	Sequence 730, App
	6	44	51.8	3396	4	US-10-094-749-921	Sequence 921, App
	7	44	51.8	421118	3	US-09-949-016-16297	Sequence 16297, A
c	8	43	50.6	170	3	US-08-818-112-47	Sequence 47, Appl
c	9	43	50.6	170	3	US-08-818-111-47	Sequence 47, Appl
c	10	43	50.6	170	3	US-09-056-556-47	Sequence 47, Appl
c	11	43	50.6	170	3	US-09-072-596-47	Sequence 47, Appl
c	12	43	50.6	170	3	US-09-072-967-47	Sequence 47, Appl
c	13	43	50.6	170	3	US-10-193-002-47	Sequence 47, Appl
c	14	43	50.6	170	3	US-10-084-843-47	Sequence 47, Appl
	15	43	50.6	490	3	US-09-401-064-317	Sequence 317, App

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
c 1	48	56.5	496	4	US-09-925-065A-393797	Sequence 393797,
c 2	48	56.5	496	5	US-09-925-065A-393797	Sequence 393797,
c 3	48	56.5	510	12	US-10-301-480-461842	Sequence 461842,
c 4	48	56.5	510	12	US-10-301-480-1075251	Sequence 1075251,
5	48	56.5	1395	7	US-10-369-493-35123	Sequence 35123, A
6	48	56.5	1395	7	US-10-369-493-38184	Sequence 38184, A
7	48	56.5	1395	7	US-10-369-493-38576	Sequence 38576, A
8	48	56.5	1407	7	US-10-369-493-35741	Sequence 35741, A
c 9	47.5	55.9	23603	8	US-10-322-281-501	Sequence 501, App
c 10	47	55.3	280	8	US-10-424-599-18629	Sequence 18629, A
c 11	47	55.3	557	4	US-09-925-065A-943541	Sequence 943541,
c 12	47	55.3	557	5	US-09-925-065A-943541	Sequence 943541,
c 13	47	55.3	588	12	US-10-301-480-407966	Sequence 407966,
c 14	47	55.3	588	12	US-10-301-480-1021375	Sequence 1021375,
c 15	47	55.3	590	4	US-09-925-065A-334432	Sequence 334432,

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	50	58.8	95963	7	US-11-021-837-39	Sequence 39, Appl
2	48	56.5	564	8	US-11-266-748A-100244	Sequence 100244,
c 3	48	56.5	564	8	US-11-266-748A-153055	Sequence 153055,
4	47	55.3	3169	6	US-10-449-902-8261	Sequence 8261, Ap
c 5	47	55.3	242825	8	US-11-266-748A-32745	Sequence 32745, A
6	46	54.1	894	8	US-11-217-529-4798	Sequence 4798, Ap
7	46	54.1	1000	8	US-11-266-748A-200641	Sequence 200641,
8	46	54.1	2217	8	US-11-217-529-80740	Sequence 80740, A
c 9	45	52.9	1394	6	US-10-953-349-7405	Sequence 7405, Ap
10	44	51.8	566	8	US-11-266-748A-53448	Sequence 53448, A
c 11	44	51.8	729	8	US-11-266-748A-298624	Sequence 298624,
12	44	51.8	1000	8	US-11-266-748A-289594	Sequence 289594,
c 13	44	51.8	1000	8	US-11-266-748A-341023	Sequence 341023,
14	44	51.8	1000	8	US-11-266-748A-400643	Sequence 400643,
c 15	44	51.8	1000	8	US-11-266-748A-471689	Sequence 471689,

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	51	60.0	488	13	CZ824672	CZ824672 OC_Ba020
2	51	60.0	729	13	CZ867792	CZ867792 OC_Ba026
3	51	60.0	753	13	CZ845422	CZ845422 OC_Ba023
c 4	51	60.0	939	10	DT801726	DT801726 126544261
5	50	58.8	454	12	CC899139	CC899139 ZMMBBb022
c 6	50	58.8	597	14	DX116259	DX116259 OG_ABa014
7	50	58.8	699	12	CC834390	CC834390 ZMMBBb018
c 8	50	58.8	882	14	DX144504	DX144504 OG_ABa017
c 9	49	57.6	134	10	DW587162	DW587162 KAAK-aac4
c 10	49	57.6	469	7	BB830496	BB830496 BB830496
11	49	57.6	774	14	CT079213	CT079213 Sus scrof
12	49	57.6	830	13	DU439822	DU439822 109842104
c 13	49	57.6	847	12	CC533118	CC533118 CH240_410
14	48.5	57.1	1044	14	CNS003JV	AL064902 Drosophil
c 15	48	56.5	488	7	BE670147	BE670147 7e30g10.x

SEQ ID NO: 2

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	60	100.0	12	2	AAW15758	Aaw15758 Peptide f
2	60	100.0	12	3	AAy87639	Aay87639 Human bra
3	41	68.3	879	8	ADY25190	Ady25190 Plant ful
4	40	66.7	453	5	ABB93808	Abb93808 Herbicida
5	40	66.7	824	5	ABB93590	Abb93590 Herbicida
6	40	66.7	824	10	AEF11437	Aef11437 A. thalia
7	39	65.0	123	7	ADD45424	Add45424 Human Pro
8	39	65.0	123	8	ADT66635	Adt66635 Human Mss
9	39	65.0	123	9	ADX07140	Adx07140 Cyclin-de
10	39	65.0	288	6	ABP57493	Abp57493 Mycobacte
11	39	65.0	349	8	ADJ50332	Adj50332 Oil-assoc
12	38	63.3	1103	8	ADN20575	Adn20575 Bacterial
13	38	63.3	2364	6	ABM04816	Abm04816 Rat micro
14	38	63.3	2459	7	ADE62725	Ade62725 Rat Prote
15	38	63.3	2459	7	ADE62713	Ade62713 Rat Prote

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	60	100.0	12	2	US-09-146-755-2	Sequence 2, Appli
2	60	100.0	12	2	US-09-817-144-2	Sequence 2, Appli
3	36	60.0	169	2	US-09-328-352-7861	Sequence 7861, Ap
4	36	60.0	402	2	US-09-270-767-61053	Sequence 61053, A
5	36	60.0	449	2	US-09-248-796A-14389	Sequence 14389, A
6	36	60.0	727	1	US-08-424-424B-2	Sequence 2, Appli
7	36	60.0	727	3	US-10-114-270-190	Sequence 190, App
8	36	60.0	727	5	PCT-US94-05363A-2	Sequence 2, Appli
9	35.5	59.2	385	2	US-09-248-796A-17673	Sequence 17673, A
10	35	58.3	86	1	US-08-320-559-33	Sequence 33, Appl
11	35	58.3	86	2	US-08-545-860D-33	Sequence 33, Appl
12	35	58.3	86	5	PCT-US94-04496-33	Sequence 33, Appl
13	35	58.3	306	2	US-09-328-352-8177	Sequence 8177, Ap
14	35	58.3	434	2	US-08-426-630-6	Sequence 6, Appli
15	35	58.3	494	2	US-09-006-636-8	Sequence 8, Appli

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	60	100.0	12	3	US-09-817-144-2	Sequence 2, Appli
2	60	100.0	12	4	US-10-642-587-2	Sequence 2, Appli
3	46	76.7	147	4	US-10-437-963-192010	Sequence 192010,
4	41	68.3	879	4	US-10-424-599-174241	Sequence 174241,
5	41	68.3	879	4	US-10-425-114-72974	Sequence 72974, A
6	40	66.7	31	4	US-10-424-599-244734	Sequence 244734,
7	39	65.0	70	4	US-10-425-115-259505	Sequence 259505,
8	39	65.0	161	4	US-10-425-115-244316	Sequence 244316,
9	39	65.0	181	4	US-10-425-115-280076	Sequence 280076,
10	39	65.0	284	4	US-10-767-701-40983	Sequence 40983, A
11	39	65.0	288	5	US-10-481-265-115	Sequence 115, App
12	39	65.0	349	4	US-10-389-566-2336	Sequence 2336, Ap
13	39	65.0	349	5	US-10-732-923-17933	Sequence 17933, A
14	39	65.0	349	6	US-11-188-298-13346	Sequence 13346, A
15	38	63.3	63	4	US-10-425-115-306376	Sequence 306376,

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	40	66.7	436	7	US-11-056-355B-90319	Sequence 90319, A
2	40	66.7	436	7	US-11-056-355B-94075	Sequence 94075, A
3	40	66.7	445	7	US-11-056-355B-90318	Sequence 90318, A
4	40	66.7	445	7	US-11-056-355B-94074	Sequence 94074, A
5	40	66.7	453	7	US-11-056-355B-90317	Sequence 90317, A
6	40	66.7	453	7	US-11-056-355B-94073	Sequence 94073, A
7	40	66.7	551	7	US-11-056-355B-47130	Sequence 47130, A
8	40	66.7	638	7	US-11-056-355B-47129	Sequence 47129, A
9	40	66.7	824	7	US-11-056-355B-47128	Sequence 47128, A
10	37	61.7	258	6	US-10-449-902-31034	Sequence 31034, A
11	37	61.7	326	6	US-10-953-349-9889	Sequence 9889, Ap
12	37	61.7	370	6	US-10-953-349-9888	Sequence 9888, Ap
13	37	61.7	406	6	US-10-953-349-9887	Sequence 9887, Ap
14	37	61.7	499	6	US-10-449-902-37996	Sequence 37996, A
15	37	61.7	825	6	US-10-449-902-46177	Sequence 46177, A

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	39	65.0	123	2	I52427	guanine-nucleotide
2	39	65.0	288	2	C70860	hypothetical prote
3	38	63.3	137	2	S64724	uxpB protein - Pse
4	38	63.3	353	2	S44162	hypothetical prote
5	38	63.3	759	2	B90520	ABC transporter at
6	38	63.3	881	2	T25786	hypothetical prote
7	38	63.3	2364	2	A56577	microtubule-associ
8	37	61.7	212	2	AG1050	conserved hypothet
9	37	61.7	290	2	S59322	hypothetical prote
10	37	61.7	359	2	S46714	hypothetical prote
11	37	61.7	402	2	AH0896	propionate kinase
12	37	61.7	484	2	G86362	beta-glucanase [im
13	37	61.7	504	2	T01603	hypothetical prote
14	37	61.7	772	2	B65167	hypothetical 88.1
15	36	60.0	146	2	C97130	probable 4-Cys fer

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	47	78.3	271	2	Q386N0_9TRYP	Q386n0 trypanosoma
2	45	75.0	745	2	Q4ING0_GIBZE	Q4ing0 gibberella
3	43	71.7	655	2	Q6P3A3_MOUSE	Q6p3a3 mus musculu
4	43	71.7	1231	2	Q3UE14_MOUSE	Q3ue14 mus musculu
5	43	71.7	1348	2	Q70X02_MOUSE	Q70x02 mus musculu
6	43	71.7	1349	2	Q7TNB8_MOUSE	Q7tnb8 mus musculu
7	42	70.0	416	2	Q4XP04_PLACH	Q4xp04 plasmodium
8	42	70.0	878	2	Q6FRP4_CANGA	Q6frp4 candida gla
9	41	68.3	175	2	Q815Y1_BACCR	Q815y1 bacillus ce
10	41	68.3	175	2	Q72Y89_BACCC1	Q72y89 bacillus ce
11	41	68.3	380	2	Q2J7J8_9ACTO	Q2j7j8 frankia sp.
12	41	68.3	652	2	Q5B9B7_EMENI	Q5b9b7 aspergillus
13	41	68.3	1131	2	Q72WT6_DESVH	Q72wt6 desulfovibr
14	40	66.7	254	2	Q6U478_9HEPC	Q6u478 hepatitis c
15	40	66.7	254	2	Q6U479_9HEPC	Q6u479 hepatitis c

NA ENCODING SEQ ID NO: 2

SUMMARIES

		% Query					
Result No.	Score	Match	Length	DB	ID	Description	
c	1	50	83.3	79534	11	CR628324	CR628324 Zebrafish
c	2	47	78.3	173849	5	AC078855	AC078855 Homo sapi
	3	47	78.3	201708	12	AC020731	AC020731 Homo sapi
c	4	46	76.7	110000	4	AP008210_020	Continuation (21 o
c	5	46	76.7	126447	4	OSJN00189	AL662985 Oryza sat
c	6	45	75.0	110000	12	AC110933_2	Continuation (3 of
c	7	45	75.0	196855	12	AC022297	AC022297 Mus muscu
c	8	45	75.0	197046	5	AC009123	AC009123 Homo sapi
	9	45	75.0	200006	12	AC166338	AC166338 Mus muscu
	10	45	75.0	204037	6	AL596207	AL596207 Mouse DNA
	11	45	75.0	210246	11	BX511081	BX511081 Zebrafish
	12	45	75.0	216522	12	AC139664	AC139664 Homo sapi
	13	45	75.0	238816	12	AC108616	AC108616 Rattus no
	14	45	75.0	252612	12	AC111263	AC111263 Rattus no
c	15	44	73.3	3340	4	AK119411	AK119411 Oryza sat

SUMMARIES

		% Query					
Result No.	Score	Match	Length	DB	ID	Description	
c	1	46	76.7	351	12	ADJ39880 Adj39880 Plant cDN	
c	2	44	73.3	1578	11	ACL28106 Acl28106 Rice abio	
c	3	44	73.3	26995	5	AAS29963 Aas29963 Human lun	
c	4	44	73.3	26995	10	ADB33300 Adb33300 Human nov	
c	5	43	71.7	213	8	ABX48104 Abx48104 Bovine ES	
c	6	43	71.7	408	8	ABX43534 Abx43534 Bovine ES	
c	7	43	71.7	185548	13	ADV34986 Adv34986 Murine cD	
	8	41	68.3	3049	13	ADX32390 Adx32390 Plant ful	
	9	40	66.7	933	13	ADX33233 Adx33233 Plant ful	
	10	40	66.7	1362	14	ADW07578 Adw07578 GTase cDN	
	11	40	66.7	1810	13	ADX31096 Adx31096 Plant ful	
	12	40	66.7	1841	12	ADO62400 Ado62400 Transcrip	
	13	40	66.7	2821	15	AEF11436 Aef11436 A. thalia	
	14	40	66.7	48995	9	ADA02579 Ada02579 Mouse Rel	
	15	40	66.7	48995	10	ADB72317 Adb72317 Mouse Rel	

SUMMARIES

CONTINUED							
Result No.	Score	% Query		DB	ID	Description	
		Match	Length				
c	1	39	65.0	275	3	US-09-513-999C-11209	Sequence 11209, A
	2	39	65.0	459	3	US-09-020-956-142	Sequence 142, App
	3	39	65.0	459	3	US-09-030-607-142	Sequence 142, App
	4	39	65.0	459	3	US-09-439-313-142	Sequence 142, App
	5	39	65.0	459	3	US-09-352-616A-142	Sequence 142, App
	6	39	65.0	459	3	US-09-232-149A-142	Sequence 142, App
	7	39	65.0	459	3	US-09-159-812-142	Sequence 142, App
	8	39	65.0	459	3	US-09-636-215-142	Sequence 142, App
	9	39	65.0	459	3	US-09-685-166A-142	Sequence 142, App
	10	39	65.0	459	3	US-09-115-453-142	Sequence 142, App
	11	39	65.0	459	3	US-09-688-489-142	Sequence 142, App
	12	39	65.0	459	3	US-09-679-426-142	Sequence 142, App
	13	39	65.0	459	3	US-09-759-143-142	Sequence 142, App
	14	39	65.0	459	3	US-09-651-236-142	Sequence 142, App
	15	39	65.0	459	3	US-09-030-606-142	Sequence 142, App

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
c 1	46	76.7	351	8	US-10-260-238-880	Sequence 880, App
c 2	46	76.7	649	8	US-10-437-963-89527	Sequence 89527, A
3	45	75.0	740	6	US-10-027-632-21907	Sequence 21907, A
4	45	75.0	740	6	US-10-027-632-148770	Sequence 148770,
5	45	75.0	740	6	US-10-027-632-148771	Sequence 148771,
6	45	75.0	740	7	US-10-027-632-21907	Sequence 21907, A
7	45	75.0	740	7	US-10-027-632-148770	Sequence 148770,
8	45	75.0	740	7	US-10-027-632-148771	Sequence 148771,
c 9	45	75.0	996	12	US-10-301-480-542262	Sequence 542262,
c 10	45	75.0	996	12	US-10-301-480-1155671	Sequence 1155671,
c 11	44	73.3	26995	3	US-09-764-878-227	Sequence 227, App
c 12	44	73.3	26995	6	US-10-079-854-227	Sequence 227, App
c 13	43	71.7	213	3	US-09-960-352-13269	Sequence 13269, A
c 14	43	71.7	408	3	US-09-960-352-8699	Sequence 8699, Ap
c 15	43	71.7	185548	6	US-10-175-523-62	Sequence 62, Appl

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	41	68.3	3065	8	US-11-216-545-7473	Sequence 7473, Ap
2	40	66.7	1362	7	US-11-056-355B-90316	Sequence 90316, A
3	40	66.7	1362	7	US-11-056-355B-94072	Sequence 94072, A
4	40	66.7	1617	6	US-10-953-349-34007	Sequence 34007, A
5	40	66.7	1617	7	US-11-056-355B-12275	Sequence 12275, A
6	40	66.7	1617	7	US-11-056-355B-19622	Sequence 19622, A
7	40	66.7	1840	7	US-11-218-305-1839	Sequence 1839, Ap
8	40	66.7	2704	7	US-11-056-355B-47127	Sequence 47127, A
c 9	39	65.0	420	8	US-11-266-748A-170341	Sequence 170341,
10	39	65.0	420	8	US-11-266-748A-245047	Sequence 245047,
c 11	39	65.0	804	8	US-11-217-529-5397	Sequence 5397, Ap
c 12	39	65.0	952	8	US-11-266-748A-228170	Sequence 228170,
13	39	65.0	1000	8	US-11-266-748A-216407	Sequence 216407,
c 14	39	65.0	1000	8	US-11-266-748A-287356	Sequence 287356,
15	39	65.0	1000	8	US-11-266-748A-338785	Sequence 338785,

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
c 1	48	80.0	500	14	DX113407	DX113407 OG_ABa013
c 2	48	80.0	663	14	DX118759	DX118759 OG_ABa014
c 3	48	80.0	695	14	DX129614	DX129614 OG_ABa015
4	48	80.0	714	14	DX124014	DX124014 OG_ABa015
c 5	48	80.0	717	13	DU159234	DU159234 OG_ABa004
c 6	48	80.0	732	14	DX135548	DX135548 OG_ABa016
7	48	80.0	741	14	DU809699	DU809699 OG_ABa010
c 8	48	80.0	754	14	DX153357	DX153357 OG_ABa019
c 9	48	80.0	766	14	DU663919	DU663919 OG_ABa007
c 10	48	80.0	767	14	DU634863	DU634863 OO_Ba014
11	48	80.0	820	13	DU161578	DU161578 OG_ABa004
c 12	47	78.3	616	11	AQ652025	AQ652025 Sheared D
c 13	46	76.7	351	13	CL967949	CL967949 OsIFCC016
c 14	46	76.7	427	1	AI001826	AI001826 ov22g11.s
15	46	76.7	561	5	CD424221	CD424221 SA1_4_B02

10/642,587

Sequence alignment A

SEQ ID NO: 1

QQBEG6

HWLF1 protein - human cytomegalovirus (strain AD169)

N;Alternate names: hypothetical protein US22

C;Species: human cytomegalovirus, human herpesvirus 5

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: F27231; S09936

R;Weston, K.; Barrell, B.G.

J. Mol. Biol. 192, 177-208, 1986

A;Title: Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.

A;Reference number: A92935; MUID:87169717; PMID:3031311

A;Accession: F27231

A;Molecule type: DNA

A;Residues: 1-593 <WES>

A;Cross-references: UNIPROT:P09722; UNIPARC:UPI0000137E39; EMBL:X04650; NID:g59801;

PIDN:CAB37114.1; PID:g4456195

A;Experimental source: strain AD169

R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;

Hutchison III, C.A.; Kouzarides, T.; Martignetti, J.A.; Preddie, E.; Satchwell, S.C.;

Tomlinson, P.; Weston, K.M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.

A;Reference number: S09749; MUID:90269039; PMID:2161319

A;Accession: S09936

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-593 <CHE>

A;Cross-references: UNIPARC:UPI0000137E39; EMBL:X17403; NID:g59591; PIDN:CAA35289.1;

PID:g1780953

A;Experimental source: strain AD169

A;Note: this sequence was submitted to the EMBL Data Library, December 1989

A;Note: this reading frame extends between two stop codons and does not begin with a start codon

C;Genetics:

A;Gene: HWLF1

C;Superfamily: cytomegalovirus HHLF5 protein

Query Match 47.1%; Score 40; DB 1; Length 593;

Best Local Similarity 57.1%; Pred. No. 68;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KAGVAFLHKNDID 15

| | | : | | | |

Db 314 KFGVVYLHKIEDSD 327

10/642,587
Sequence alignment B
SEQ ID NO: 2
A32183
tropomyosin TPM1 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein N2332; protein YNL079c
C;Species: *Saccharomyces cerevisiae*
C;Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #text_change 31-Dec-2004
C;Accession: A32183; S53899; S63011; S63018; S63928
R;Liu, H.; Bretscher, A.
Cell 57, 233-242, 1989
A;Title: Disruption of the single tropomyosin gene in yeast results in the disappearance of actin cables from the cytoskeleton.
A;Reference number: A32183; MUID:89195234; PMID:2649250
A;Accession: A32183
A;Molecule type: DNA
A;Residues: 1-199 <LIU>
A;Cross-references: UNIPROT:P17536; UNIPARC:UPI0000137254; EMBL:M25501; NID:g173037; PIDN:AAA35174.1; PID:g173038
R;Poehlmann, R.; Philippsen, P.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53896
A;Accession: S53899
A;Molecule type: DNA
A;Residues: 1-199 <POE>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
R;Poehlmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62997
A;Accession: S63011
A;Molecule type: DNA
A;Residues: 1-199 <POW>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL079c
A;Experimental source: strain S288C
R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63018
A;Accession: S63018
A;Molecule type: DNA
A;Residues: 1-199 <SOL>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL079c
A;Experimental source: strain S288C
R;Poehlmann, R.; Philippsen, P.
Yeast 12, 391-402, 1996
A;Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12 new open reading frames (ORFs) and an ancient duplication of six ORFs.
A;Reference number: S63925; MUID:96267764; PMID:8701611
A;Accession: S63928
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-199 <POF>
A;Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics:
A;Gene: SGD:TPM1
A;Cross-references: SGD:S0005023; MIPS:YNL079c
A;Map position: 14L
C;Superfamily: slime mold ribozyme I
C;Keywords: coiled coil; cytoskeleton

Query Match 60.0%; Score 36; DB 2; Length 199;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GLSDGSNTESD 11
||| |
Db 63 GLSDSKQTEQD 73